

Figure 1  
Interleukin-21

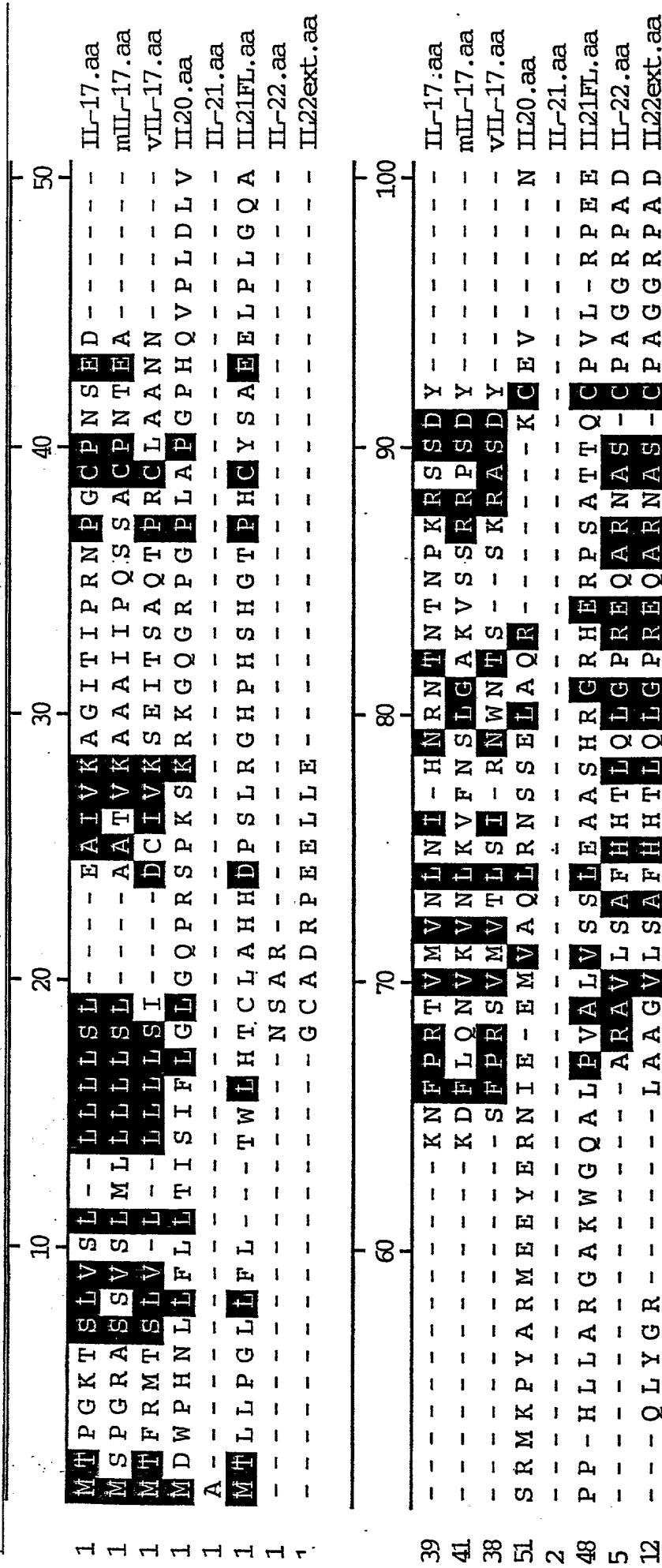
1 GGCACGAGTGGACACGGATGAGGACCGCTATCCACAGAACGCTGGCCTTCGCCAGTCCT 60  
 1 A R V D T D E D R Y P Q K L A F A E C L 20  
 Domain I Domain II  
  
 61 GTGCAGAGGCTGTATCGATGCACGGACGGCCGAGACAGCTGCCTCAACTCCGTGCG 120  
 21 C R G C I D A R T G R E T A A L N S V R 40  
 Domain II  
  
 121 GCTGCTCCAGAGCCTGCTGGTGCCTGCCGCCGCCCCCTGCTCCCGCACGGCTGGGGCT 180  
 41 L L Q S L L V L R R R P C S R D G S G L 60  
 Domain III  
  
 181 CCCCCACACCTGGGCTTGGCTTCCACACCGAGTTCACTCCACGTCCCCGTGGCTGGAC 240  
 61 P T P G A F A F H T E F I H V P V G C T 80  
 Domain IV  
  
 241 CTGGTGCTGCCCGTTCAAGTGTGACGCCAAGGCCGTGGGCCCTTAGACTGGACACGT 300  
 81 C V L P R S V 87  
 Domain IV  
  
 301 GTGCTCCCCAGAGGGCACCCCTATTTATGIGTATTTATTGTTATTTATATGCCCTCCCC 360  
  
 361 AACACTACCCCTGGGCTGGCATTCCTGGCTGGAGGACAGCCCCCACTGGCTCTC 420  
  
 421 CTCACTCCAGCCTCACTAGTGGGGTWGAAGGAGCTCACCCCTCTCCAGCCCTAA 480  
  
 481 AGCTGCAGAAAAGGTGTCACACGGCTGCCGTACCTTGGYTCCCTGCCGTCCGGCT 540  
  
 541 TCCCTTACCCATCACTGGCTCAGGCCCCCGCAGGCTGCCCTTCCAAACCTCCCTGG 600  
  
 601 AGTACCCCTGTTCTAAACAATTATTAAGTGTACGTGTATTAAACTGATGAACAC 660  
  
 661 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 705

Figure 2A  
Interleukin-22

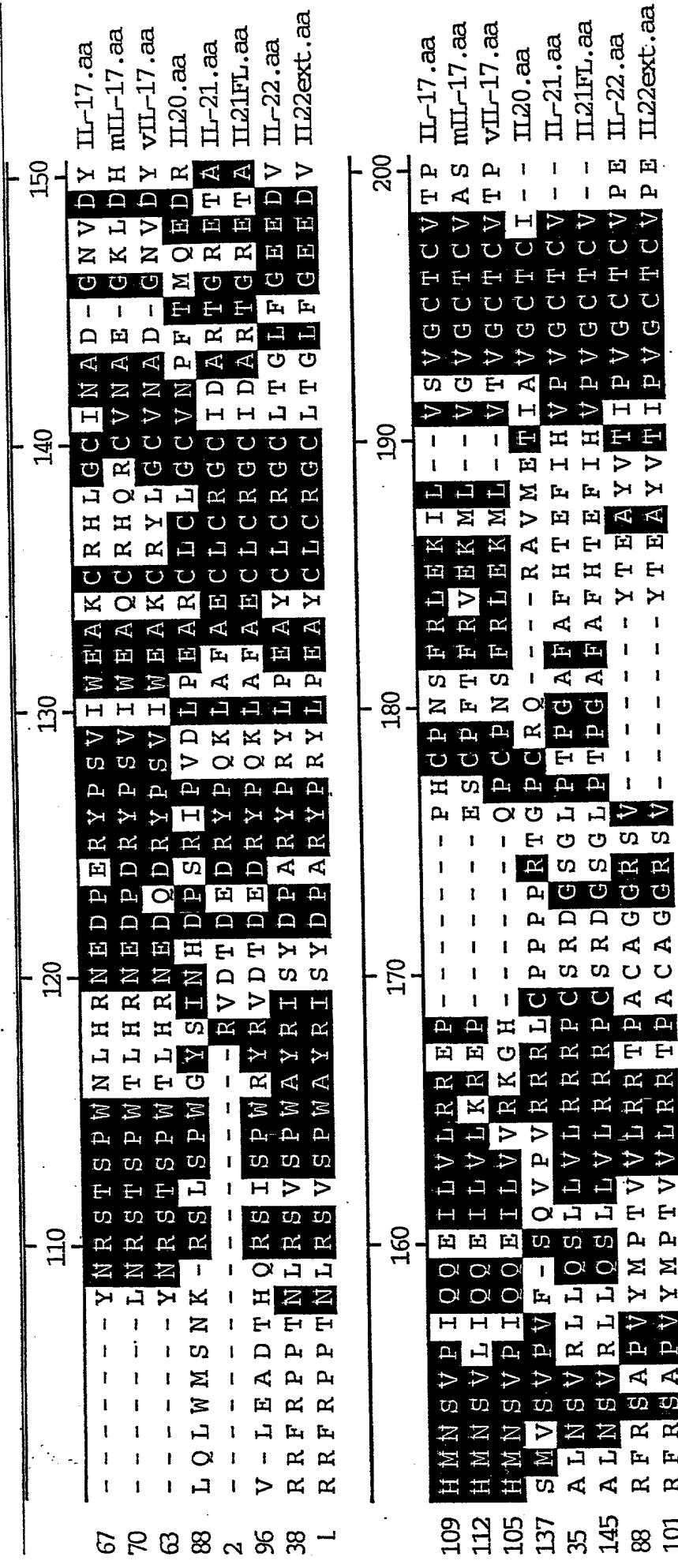
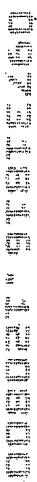
1	GGAATTGGCACCGAGCTCGTGCCTGCTCAGTGCCCTCCACACACGCTGCAGCTGGGC	60
1	N S A R A R A V L S A F H H T L Q L G P	20
	#	
61	CGCGTGAGCAGGCCGCAACCGAGCTGCCGGCAGGGGAGGCCGACCGCCGCT	120
21	R E Q A R N A S C P A G G R P A D R R F	40
121	TCCGGCCGCCACCAACCTGGCAGCGTGTGCCCTGGCCTACAGAAATCTCCTACGACC	180
41	R P P T N L R S V S P W A Y R I S Y D P	60
	Domain I	
181	CGCGGAGGTACCCCAGGTACCTGGCTGAAGCCTACTGCCGTGCCGGGCTGCCGTACCG	240
61	<u>A R Y P R Y L P E A Y C L C R G C L T G</u>	80
	Domain I	Domain II
241	GGCTGTTCGGCGAGGAGGACGTGCCCTTCCGAGCGCCCCCTGCTACATGCCAACCGTCG	300
81	L F G E E D V R F R S A P V Y M P T V V	100
	Domain III	
301	TCCGTGCCGCACCCCGCCTGGCCGGGGCGTCCGTCTACACCGAGGCCTACGTCA	360
101	<u>L R R T P A C A G G R S V Y T E A Y V T</u>	120
	Domain III	
361	CCATCCCCGTGGCTGACCTGGCTCCCGAGCGGAGAAGGACGCAGACGGCATCAACT	420
121	<u>I P V G C T C V P E P E K D A D S I N S</u>	140
	Domain IV	
421	CCAGCATCGACAAACAGGGCCCAAGCTCCGTGGCCCCAACGACGCCGGCTGGCC	480
141	S I D K Q G A K L L L G P N D A P A G P	160
481	CCTGAGGCCGGTCCCTGCCCGGGAGGTCTCCCGGCCATCCGAGGCCAACGCTG	540
541	GAGCCGCCTGGAGGGCTCGTCGGGACCTCTGAAGAGAGTCACCGAGCAAACCAAGTG	600
601	CCGGAGCACCAGGCCGCTTCCATGGAGACTCGTAAGCAGCTTCATCTGACACGGCA	660
661	TCCCTGGCTTGCTTTAGCTACAAGCAAGCAGCGTGGCTGGAACCTGATGGAAACGACC	720
721	CGGCACGGCATTCTGTGTGGGCCGATGGAGGGTTGGAAAAGTTACGGAGGCTCC	780
781	CTGAGGAGCCTCTCAGATCGGCTGCTGGGGTGCAGGGCGTGAATCACCCTGGTGCTT	840
841	GCCAAAGAGATAGGGACCCATATGCTTTAAAGCAATCTAAAAATAATAAGTATAG	900

Figure 2B  
Interleukin-22

092346-120800  
901 CGACTATATACTACTTTAAAATCAACTGTTTGAATAGAGGCAGAGCTATTTATATT 960  
961 ATCAAATGAGAGCTACTCTGTTACATTCTTAACATATAAACATCGTTTTACTCTTC 1020  
1021 TGGTAGAAATTTTTAAAGCATAATTGGAATCCTTGGATAAATTTGTAGCTGGTACACTC 1080  
1081 TGGCCTGGGTCTCTGAATTAGCCTGTCACCGATGGCTGACTGATGAAATGGACACGCT 1140  
1141 CATCTGACCCACTCTCCCTCCACTGAAGGTCTCACGGGCCCTCAGGTGGACCAAAGGG 1200  
1201 ATGCACAGGCGGCTCGCATGCCAGGGCCAGCTAAGAGTCCAAAGATCTCAGATTGG 1260  
1261 TTTTAGTCATGAATAACATAAACAGTCTCAAACCTCGCACAAATTTTCCCCCTTTTGAAAG 1320  
1321 CCACTGGGCCAATTGTGGTTAAGAGGTGGTGGATAAGAAGTGGAACGTGACATCTT 1380  
1381 GCCAGTTGTCAAGAAGATCCAAGCAGGTATTGGCTTAGTTGTAAGGGCTTAGGATCAGG 1440  
1441 CTGAATATGAGGACAAGTGGGCCACGTTAGCATCTGCAGAGATCAATCTGGAGGCTCT 1500  
1501 GTTTCTGCATTCTGCCACGGAGAGCTAGGTCTTGATCTTTCTTTAGATTGAAAGTCGT 1560  
1561 CTCTGAACACAATTATTTGTAAGTTAGTAGTTCTTTTAAATCATTAAAAGAGGCTT 1620  
1621 GCTGAAAAAAAAAAAAAAA 1642



**Figure 3A**



**Figure 3B**

CHARGE STATE

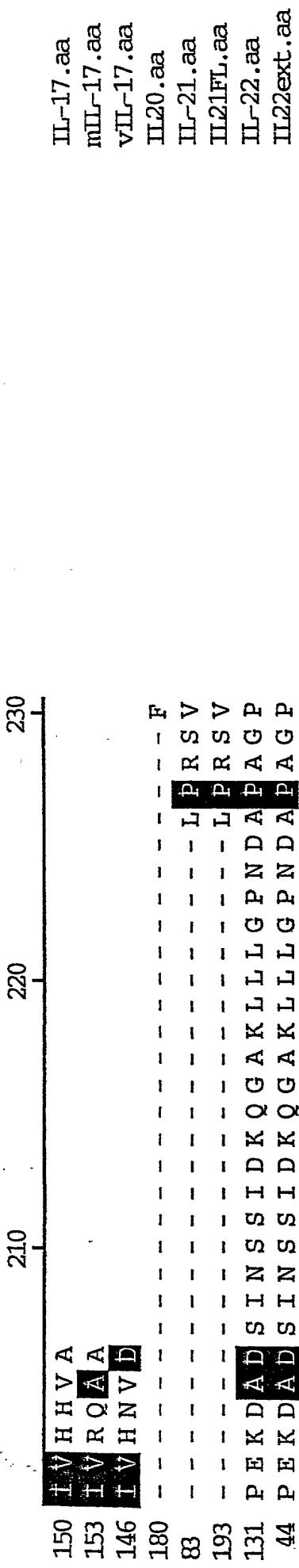
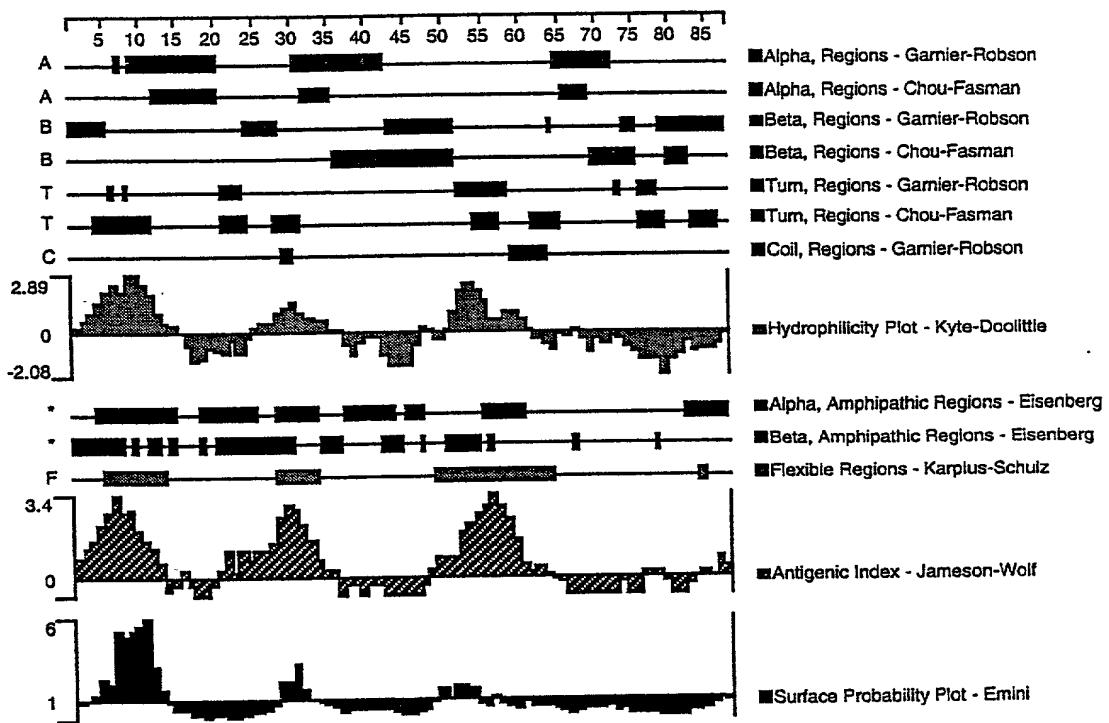


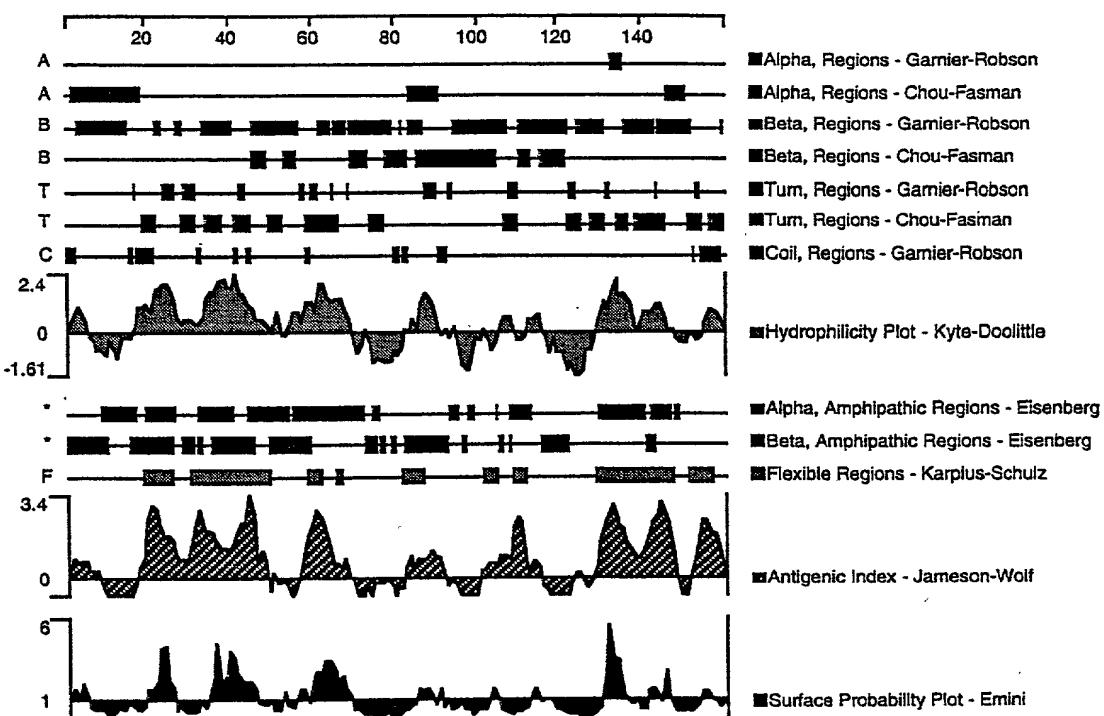
Figure 3C

**Figure 4**  
**Interleukin-21 Polypeptide Analysis**



0 9 7 2 3 1 8 1 6 1 4 2 0 0 0 0 0 0

**Figure 5**  
**Interleukin-22 Polypeptide Analysis**

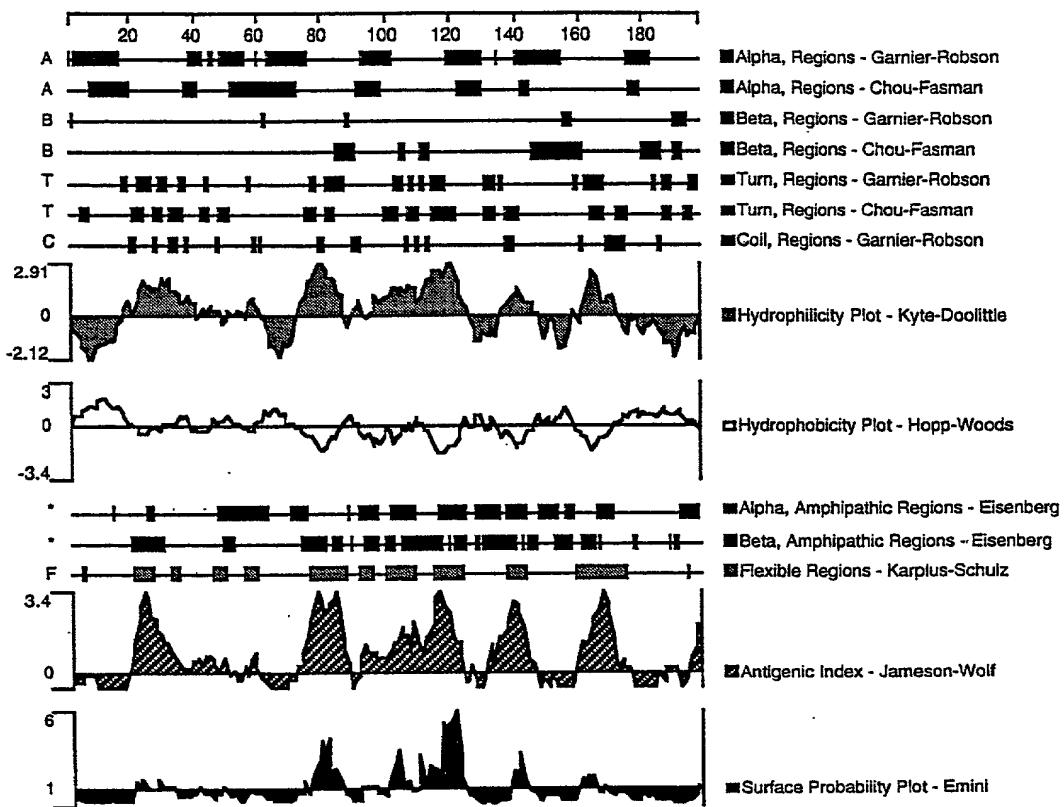


**Figure 6A**  
**Interleukin-21**

1	GCTCCAAGCCCAGCCTGCCCGCTGCCGCCACCATGACGCTCCCTCCCCGCCCTCCGTGTTT	60
1	<u>M T L L P G L L F</u>	9
61	CTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGGGCACCCCCAC	120
10	<u>L T W L H T C L A H H D P S L R G H P H</u>	29
121	AGTCACGGTACCCCACACTGCTACTCGGCTGAGGAAC TGCCCTCGGCCAGGCCCCCA	180
30	<u>S H G T P H C Y S A E E L P L G Q A P P</u>	49
	Domain V	
181	CACCTGCTGGCTCGAGGTGCCAAGTGGGGCAGGCTTGCTCTGTAGCCCTGGTGTCCAGC	240
50	<u>H L L A R G A K W G Q A L P V A L V S S</u>	69
	Domain VI	
241	CTGGAGGCAGCAAGCCACAGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCCG	300
70	<u>L E A A S H R G R H E R P S A T T Q C P</u>	89
301	GTGCTCGGCCGGAGGAGGTGGAGGCAGACACCCACCAGCGCTCCATCTCACCTGG	360
90	<u>V L R P E E V L E A D T H Q R S I S P W</u>	109
	Domain VII	
361	AGATACCGGGTGGACACGGATGAGGACCGCTATCCACAGAACGCTGGCCTTCGCCAGTG	420
110	<u>R Y R V D T D E D R Y P Q K L A F A E C</u>	129
	Domain I	Domain II
421	CTGTGCAGAGGCTGTATCGATGCACGGACGGCCGGCGAGACAGCTGCGCTCAACTCCGT	480
130	<u>L C R G C I D A R T G R E T A A L N S V</u>	149
	Domain II	
481	CGGCTGCTCCAGAGCCTGCTGGTGCTGCCGCCGGCCCTGCTCCCGCAGGGCTGGGG	540
150	<u>R L L Q S L L V L R R R P C S R D G S G</u>	169
	Domain III	
541	CTCCCCACACCTGGGGCTTGGCTCCACACCGAGTTCAATCCACGTCCCCGTGGCTGC	600
170	<u>L P T P G A F A F H T E F I H V P V G C</u>	189
	Domain IV	
601	ACCTGCGTGCTGCCCGTTCACTGTGACCGCCAAGGCCGTGGGGCCCTAGACTGGACAC	660
190	<u>T C V L P R S V</u>	197
	Domain IV	
661	GTGTGCTCCCCAGAGGGCACCCCTATTTATGTGTATTTATGGTATTTATATGCTCCC	720
721	CCAAACACTACCCCTGGGGCTGGGATTCCCCGTGTCTGGAGGACAGCCCCCACTGGTC	780

Figure 6B  
Interleukin-21

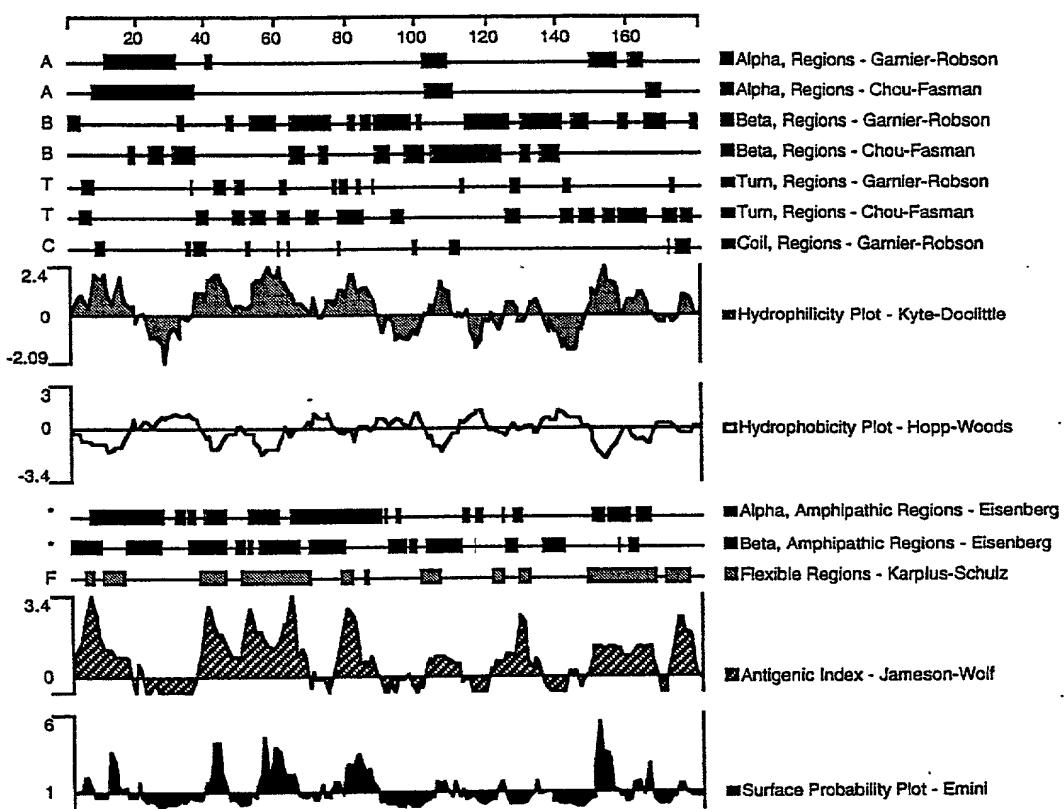
**Figure 7**  
**Interleukin-21 Polypeptide Analysis**



**Figure 8**  
**Interleukin-22**

1	GGCTCGCGGACCGCCGGAGGAGCTACTGGACCAGCTGTACGGGCCCTGGCGGCCGC	60
1	G C A D R P E E L L E Q L Y G R L <u>A A G</u>	20
	CD-VI	
	#	
61	GTGCTCAGTGCCTTCCACCAACACGCTGCAGCTGGGGCCGCGTGAGCAGGCCGCAACGCG	120
21	<u>V L S</u> A F H H T L Q L G P R E Q A R N A	40
	CD-VI	
121	AGCTGCCCGCAGGGGGCAGGCCGCCCAGGCCGCTTCCGCCGCCACCAACCTGCGC	180
41	S C P A G G R P A D R R F R P P T N L <u>R</u>	60
181	AGCGTGTGCCCTGGGCTACAGAATCTCCTACGACCCGGGAGGTACCCAGGTACCTG	240
61	<u>S V S P W A Y R I S Y D P A R Y P R Y L</u>	80
	CD-VII	
	CD-I	
241	CCTGAAGCCTACTGCCTGTGCCGGGGCTGCCTGACCGGGCTGTCGGCGAGGAGCTG	300
81	P E A Y C L C R G C L T G L F G E E D V	100
	CD-II	
301	CGCTTCCGAGGCCCTGTCTACATGCCAACGTCGTCTGCCGCCACCCCGCCTGC	360
101	R F R S A P V Y M P T <u>V V L R R T P A C</u>	120
	CD-III	
361	GCCGGCGCCGTTCCGCTACACCGAGGCCTACGTCAACCATCCCCGTGGCTGCACCTGC	420
121	A G G R S V Y T E A Y V T <u>I P V G C T C</u>	140
	CD-IV	
	#	
421	GTCCCCGACCCGGAGAAGGACGCCAGACAGCATCAACTCCAGCATCGACAAACAGGGCGCC	480
141	<u>V P E P E K D A D S I N S S I D K Q G A</u>	160
	CD-IV	
481	AAGCTCCCTGCTGGGCCCCAACGACGCCCGCTGGCCCTGA	522
161	K L L L G P N D A P A G P	174

**Figure 9**  
**Interleukin-22 Polypeptide Analysis**



0 9 8 3 1 6 3 5 5 4 1 0 0 8 0 0 0